



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:21 AM UTC

PDB ID : 7RFF / pdb_00007rff
EMDB ID : EMD-24440
Title : HUMAN RETINAL VARIANT IMPDH1(595) TREATED WITH ATP;
INTERFACE-CENTERED
Authors : Burrell, A.L.; Kollman, J.M.
Deposited on : 2021-07-14
Resolution : 2.70 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

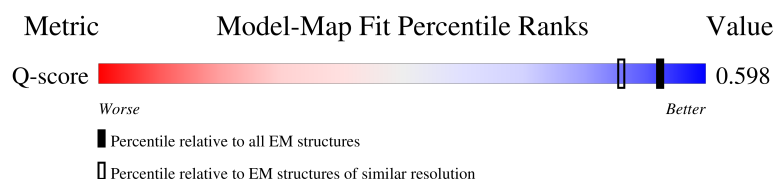
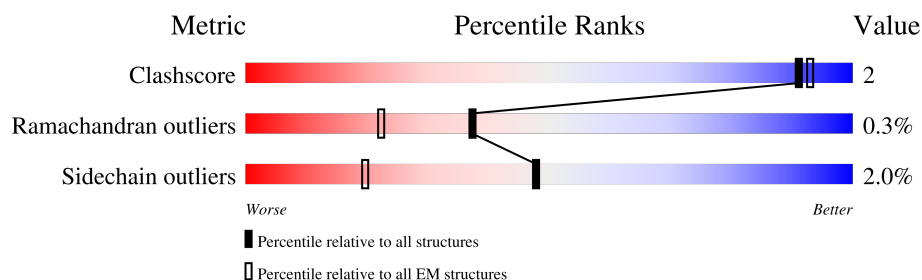
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	621	
1	B	621	
1	C	621	
1	D	621	

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Mol	Chain	Length	Quality of chain
1	E	621	5% 53% 45%
1	F	621	5% 53% 45%
1	G	621	5% 53% 45%
1	H	621	5% 51% 45%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 41000 atoms, of which 20600 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Isoform 5 of Inosine-5'-monophosphate dehydrogenase 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	B	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	C	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	D	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	E	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	F	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	G	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		
1	H	339	Total	C	H	N	O	S	0	0
			5125	1612	2575	438	483	17		

There are 296 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	510	THR	-	expression tag	UNP P20839-5
A	511	PHE	-	expression tag	UNP P20839-5
A	512	LEU	-	expression tag	UNP P20839-5
A	513	PRO	-	expression tag	UNP P20839-5
A	514	PHE	-	expression tag	UNP P20839-5
A	515	THR	-	expression tag	UNP P20839-5
A	516	LYS	-	expression tag	UNP P20839-5
A	517	SER	-	expression tag	UNP P20839-5
A	518	GLY	-	expression tag	UNP P20839-5
A	519	CYS	-	expression tag	UNP P20839-5
A	520	THR	-	expression tag	UNP P20839-5
A	521	GLU	-	expression tag	UNP P20839-5
A	522	ASP	-	expression tag	UNP P20839-5
A	523	SER	-	expression tag	UNP P20839-5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	524	GLY	-	expression tag	UNP P20839-5
A	525	GLY	-	expression tag	UNP P20839-5
A	526	GLY	-	expression tag	UNP P20839-5
A	527	ARG	-	expression tag	UNP P20839-5
A	528	GLY	-	expression tag	UNP P20839-5
A	529	GLY	-	expression tag	UNP P20839-5
A	530	GLY	-	expression tag	UNP P20839-5
A	531	GLY	-	expression tag	UNP P20839-5
A	532	ASP	-	expression tag	UNP P20839-5
A	533	ALA	-	expression tag	UNP P20839-5
A	534	PRO	-	expression tag	UNP P20839-5
A	535	GLN	-	expression tag	UNP P20839-5
A	536	CYS	-	expression tag	UNP P20839-5
A	537	PRO	-	expression tag	UNP P20839-5
A	538	LEU	-	expression tag	UNP P20839-5
A	539	LEU	-	expression tag	UNP P20839-5
A	540	GLY	-	expression tag	UNP P20839-5
A	541	THR	-	expression tag	UNP P20839-5
A	542	ALA	-	expression tag	UNP P20839-5
A	543	SER	-	expression tag	UNP P20839-5
A	544	LEU	-	expression tag	UNP P20839-5
A	545	HIS	-	expression tag	UNP P20839-5
A	546	ASN	-	expression tag	UNP P20839-5
B	510	THR	-	expression tag	UNP P20839-5
B	511	PHE	-	expression tag	UNP P20839-5
B	512	LEU	-	expression tag	UNP P20839-5
B	513	PRO	-	expression tag	UNP P20839-5
B	514	PHE	-	expression tag	UNP P20839-5
B	515	THR	-	expression tag	UNP P20839-5
B	516	LYS	-	expression tag	UNP P20839-5
B	517	SER	-	expression tag	UNP P20839-5
B	518	GLY	-	expression tag	UNP P20839-5
B	519	CYS	-	expression tag	UNP P20839-5
B	520	THR	-	expression tag	UNP P20839-5
B	521	GLU	-	expression tag	UNP P20839-5
B	522	ASP	-	expression tag	UNP P20839-5
B	523	SER	-	expression tag	UNP P20839-5
B	524	GLY	-	expression tag	UNP P20839-5
B	525	GLY	-	expression tag	UNP P20839-5
B	526	GLY	-	expression tag	UNP P20839-5
B	527	ARG	-	expression tag	UNP P20839-5
B	528	GLY	-	expression tag	UNP P20839-5

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Chain	Residue	Modelled	Actual	Comment	Reference
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B	530	GLY	-	expression tag	UNP P20839-5
B	531	GLY	-	expression tag	UNP P20839-5
B	532	ASP	-	expression tag	UNP P20839-5
B	533	ALA	-	expression tag	UNP P20839-5
B	534	PRO	-	expression tag	UNP P20839-5
B	535	GLN	-	expression tag	UNP P20839-5
B	536	CYS	-	expression tag	UNP P20839-5
B	537	PRO	-	expression tag	UNP P20839-5
B	538	LEU	-	expression tag	UNP P20839-5
B	539	LEU	-	expression tag	UNP P20839-5
B	540	GLY	-	expression tag	UNP P20839-5
B	541	THR	-	expression tag	UNP P20839-5
B	542	ALA	-	expression tag	UNP P20839-5
B	543	SER	-	expression tag	UNP P20839-5
B	544	LEU	-	expression tag	UNP P20839-5
B	545	HIS	-	expression tag	UNP P20839-5
B	546	ASN	-	expression tag	UNP P20839-5
C	510	THR	-	expression tag	UNP P20839-5
C	511	PHE	-	expression tag	UNP P20839-5
C	512	LEU	-	expression tag	UNP P20839-5
C	513	PRO	-	expression tag	UNP P20839-5
C	514	PHE	-	expression tag	UNP P20839-5
C	515	THR	-	expression tag	UNP P20839-5
C	516	LYS	-	expression tag	UNP P20839-5
C	517	SER	-	expression tag	UNP P20839-5
C	518	GLY	-	expression tag	UNP P20839-5
C	519	CYS	-	expression tag	UNP P20839-5
C	520	THR	-	expression tag	UNP P20839-5
C	521	GLU	-	expression tag	UNP P20839-5
C	522	ASP	-	expression tag	UNP P20839-5
C	523	SER	-	expression tag	UNP P20839-5
C	524	GLY	-	expression tag	UNP P20839-5
C	525	GLY	-	expression tag	UNP P20839-5
C	526	GLY	-	expression tag	UNP P20839-5
C	527	ARG	-	expression tag	UNP P20839-5
C	528	GLY	-	expression tag	UNP P20839-5
C	529	GLY	-	expression tag	UNP P20839-5
C	530	GLY	-	expression tag	UNP P20839-5
C	531	GLY	-	expression tag	UNP P20839-5
C	532	ASP	-	expression tag	UNP P20839-5
C	533	ALA	-	expression tag	UNP P20839-5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	534	PRO	-	expression tag	UNP P20839-5
C	535	GLN	-	expression tag	UNP P20839-5
C	536	CYS	-	expression tag	UNP P20839-5
C	537	PRO	-	expression tag	UNP P20839-5
C	538	LEU	-	expression tag	UNP P20839-5
C	539	LEU	-	expression tag	UNP P20839-5
C	540	GLY	-	expression tag	UNP P20839-5
C	541	THR	-	expression tag	UNP P20839-5
C	542	ALA	-	expression tag	UNP P20839-5
C	543	SER	-	expression tag	UNP P20839-5
C	544	LEU	-	expression tag	UNP P20839-5
C	545	HIS	-	expression tag	UNP P20839-5
C	546	ASN	-	expression tag	UNP P20839-5
D	510	THR	-	expression tag	UNP P20839-5
D	511	PHE	-	expression tag	UNP P20839-5
D	512	LEU	-	expression tag	UNP P20839-5
D	513	PRO	-	expression tag	UNP P20839-5
D	514	PHE	-	expression tag	UNP P20839-5
D	515	THR	-	expression tag	UNP P20839-5
D	516	LYS	-	expression tag	UNP P20839-5
D	517	SER	-	expression tag	UNP P20839-5
D	518	GLY	-	expression tag	UNP P20839-5
D	519	CYS	-	expression tag	UNP P20839-5
D	520	THR	-	expression tag	UNP P20839-5
D	521	GLU	-	expression tag	UNP P20839-5
D	522	ASP	-	expression tag	UNP P20839-5
D	523	SER	-	expression tag	UNP P20839-5
D	524	GLY	-	expression tag	UNP P20839-5
D	525	GLY	-	expression tag	UNP P20839-5
D	526	GLY	-	expression tag	UNP P20839-5
D	527	ARG	-	expression tag	UNP P20839-5
D	528	GLY	-	expression tag	UNP P20839-5
D	529	GLY	-	expression tag	UNP P20839-5
D	530	GLY	-	expression tag	UNP P20839-5
D	531	GLY	-	expression tag	UNP P20839-5
D	532	ASP	-	expression tag	UNP P20839-5
D	533	ALA	-	expression tag	UNP P20839-5
D	534	PRO	-	expression tag	UNP P20839-5
D	535	GLN	-	expression tag	UNP P20839-5
D	536	CYS	-	expression tag	UNP P20839-5
D	537	PRO	-	expression tag	UNP P20839-5
D	538	LEU	-	expression tag	UNP P20839-5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	539	LEU	-	expression tag	UNP P20839-5
D	540	GLY	-	expression tag	UNP P20839-5
D	541	THR	-	expression tag	UNP P20839-5
D	542	ALA	-	expression tag	UNP P20839-5
D	543	SER	-	expression tag	UNP P20839-5
D	544	LEU	-	expression tag	UNP P20839-5
D	545	HIS	-	expression tag	UNP P20839-5
D	546	ASN	-	expression tag	UNP P20839-5
E	510	THR	-	expression tag	UNP P20839-5
E	511	PHE	-	expression tag	UNP P20839-5
E	512	LEU	-	expression tag	UNP P20839-5
E	513	PRO	-	expression tag	UNP P20839-5
E	514	PHE	-	expression tag	UNP P20839-5
E	515	THR	-	expression tag	UNP P20839-5
E	516	LYS	-	expression tag	UNP P20839-5
E	517	SER	-	expression tag	UNP P20839-5
E	518	GLY	-	expression tag	UNP P20839-5
E	519	CYS	-	expression tag	UNP P20839-5
E	520	THR	-	expression tag	UNP P20839-5
E	521	GLU	-	expression tag	UNP P20839-5
E	522	ASP	-	expression tag	UNP P20839-5
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E	536	CYS	-	expression tag	UNP P20839-5
E	537	PRO	-	expression tag	UNP P20839-5
E	538	LEU	-	expression tag	UNP P20839-5
E	539	LEU	-	expression tag	UNP P20839-5
E	540	GLY	-	expression tag	UNP P20839-5
E	541	THR	-	expression tag	UNP P20839-5
E	542	ALA	-	expression tag	UNP P20839-5
E	543	SER	-	expression tag	UNP P20839-5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	544	LEU	-	expression tag	UNP P20839-5
E	545	HIS	-	expression tag	UNP P20839-5
E	546	ASN	-	expression tag	UNP P20839-5
F	510	THR	-	expression tag	UNP P20839-5
F	511	PHE	-	expression tag	UNP P20839-5
F	512	LEU	-	expression tag	UNP P20839-5
F	513	PRO	-	expression tag	UNP P20839-5
F	514	PHE	-	expression tag	UNP P20839-5
F	515	THR	-	expression tag	UNP P20839-5
F	516	LYS	-	expression tag	UNP P20839-5
F	517	SER	-	expression tag	UNP P20839-5
F	518	GLY	-	expression tag	UNP P20839-5
F	519	CYS	-	expression tag	UNP P20839-5
F	520	THR	-	expression tag	UNP P20839-5
F	521	GLU	-	expression tag	UNP P20839-5
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F	523	SER	-	expression tag	UNP P20839-5
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F	525	GLY	-	expression tag	UNP P20839-5
F	526	GLY	-	expression tag	UNP P20839-5
F	527	ARG	-	expression tag	UNP P20839-5
F	528	GLY	-	expression tag	UNP P20839-5
F	529	GLY	-	expression tag	UNP P20839-5
F	530	GLY	-	expression tag	UNP P20839-5
F	531	GLY	-	expression tag	UNP P20839-5
F	532	ASP	-	expression tag	UNP P20839-5
F	533	ALA	-	expression tag	UNP P20839-5
F	534	PRO	-	expression tag	UNP P20839-5
F	535	GLN	-	expression tag	UNP P20839-5
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F	541	THR	-	expression tag	UNP P20839-5
F	542	ALA	-	expression tag	UNP P20839-5
F	543	SER	-	expression tag	UNP P20839-5
F	544	LEU	-	expression tag	UNP P20839-5
F	545	HIS	-	expression tag	UNP P20839-5
F	546	ASN	-	expression tag	UNP P20839-5
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G	511	PHE	-	expression tag	UNP P20839-5

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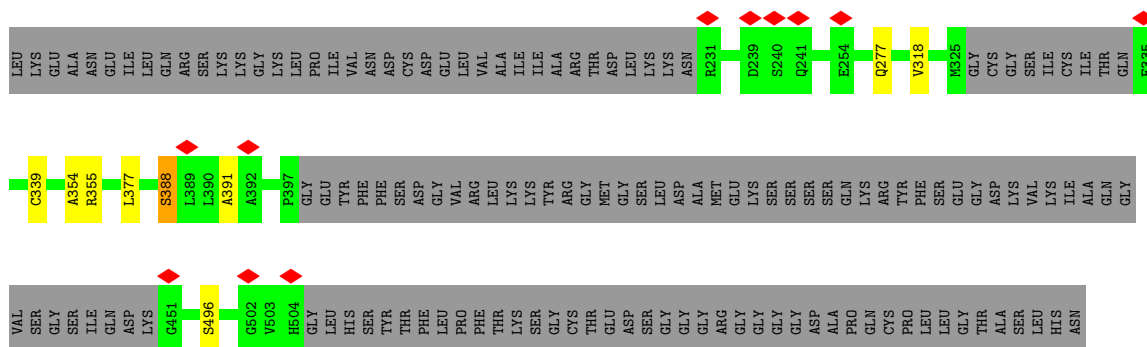
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Chain	Residue	Modelled	Actual	Comment	Reference
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G	516	LYS	-	expression tag	UNP P20839-5
G	517	SER	-	expression tag	UNP P20839-5
G	518	GLY	-	expression tag	UNP P20839-5
G	519	CYS	-	expression tag	UNP P20839-5
G	520	THR	-	expression tag	UNP P20839-5
G	521	GLU	-	expression tag	UNP P20839-5
G	522	ASP	-	expression tag	UNP P20839-5
G	523	SER	-	expression tag	UNP P20839-5
G	524	GLY	-	expression tag	UNP P20839-5
G	525	GLY	-	expression tag	UNP P20839-5
G	526	GLY	-	expression tag	UNP P20839-5
G	527	ARG	-	expression tag	UNP P20839-5
G	528	GLY	-	expression tag	UNP P20839-5
G	529	GLY	-	expression tag	UNP P20839-5
G	530	GLY	-	expression tag	UNP P20839-5
G	531	GLY	-	expression tag	UNP P20839-5
G	532	ASP	-	expression tag	UNP P20839-5
G	533	ALA	-	expression tag	UNP P20839-5
G	534	PRO	-	expression tag	UNP P20839-5
G	535	GLN	-	expression tag	UNP P20839-5
G	536	CYS	-	expression tag	UNP P20839-5
G	537	PRO	-	expression tag	UNP P20839-5
G	538	LEU	-	expression tag	UNP P20839-5
G	539	LEU	-	expression tag	UNP P20839-5
G	540	GLY	-	expression tag	UNP P20839-5
G	541	THR	-	expression tag	UNP P20839-5
G	542	ALA	-	expression tag	UNP P20839-5
G	543	SER	-	expression tag	UNP P20839-5
G	544	LEU	-	expression tag	UNP P20839-5
G	545	HIS	-	expression tag	UNP P20839-5
G	546	ASN	-	expression tag	UNP P20839-5
H	510	THR	-	expression tag	UNP P20839-5
H	511	PHE	-	expression tag	UNP P20839-5
H	512	LEU	-	expression tag	UNP P20839-5
H	513	PRO	-	expression tag	UNP P20839-5
H	514	PHE	-	expression tag	UNP P20839-5
H	515	THR	-	expression tag	UNP P20839-5
H	516	LYS	-	expression tag	UNP P20839-5

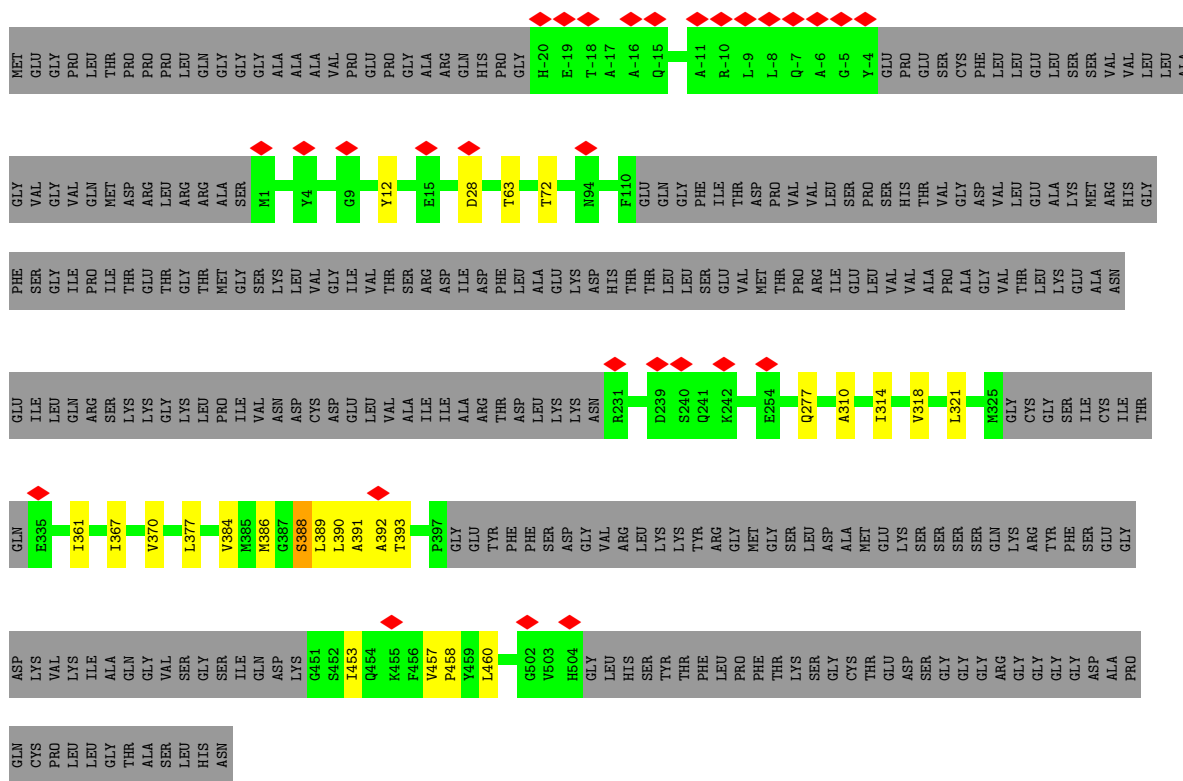
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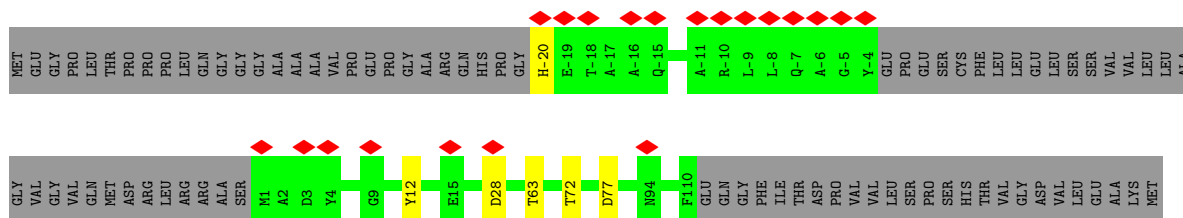
Chain	Residue	Modelled	Actual	Comment	Reference
H	517	SER	-	expression tag	UNP P20839-5
H	518	GLY	-	expression tag	UNP P20839-5
H	519	CYS	-	expression tag	UNP P20839-5
H	520	THR	-	expression tag	UNP P20839-5
H	521	GLU	-	expression tag	UNP P20839-5
H	522	ASP	-	expression tag	UNP P20839-5
H	523	SER	-	expression tag	UNP P20839-5
H	524	GLY	-	expression tag	UNP P20839-5
H	525	GLY	-	expression tag	UNP P20839-5
H	526	GLY	-	expression tag	UNP P20839-5
H	527	ARG	-	expression tag	UNP P20839-5
H	528	GLY	-	expression tag	UNP P20839-5
H	529	GLY	-	expression tag	UNP P20839-5
H	530	GLY	-	expression tag	UNP P20839-5
H	531	GLY	-	expression tag	UNP P20839-5
H	532	ASP	-	expression tag	UNP P20839-5
H	533	ALA	-	expression tag	UNP P20839-5
H	534	PRO	-	expression tag	UNP P20839-5
H	535	GLN	-	expression tag	UNP P20839-5
H	536	CYS	-	expression tag	UNP P20839-5
H	537	PRO	-	expression tag	UNP P20839-5
H	538	LEU	-	expression tag	UNP P20839-5
H	539	LEU	-	expression tag	UNP P20839-5
H	540	GLY	-	expression tag	UNP P20839-5
H	541	THR	-	expression tag	UNP P20839-5
H	542	ALA	-	expression tag	UNP P20839-5
H	543	SER	-	expression tag	UNP P20839-5
H	544	LEU	-	expression tag	UNP P20839-5
H	545	HIS	-	expression tag	UNP P20839-5
H	546	ASN	-	expression tag	UNP P20839-5



- Molecule 1: Isoform 5 of Inosine-5'-monophosphate dehydrogenase 1



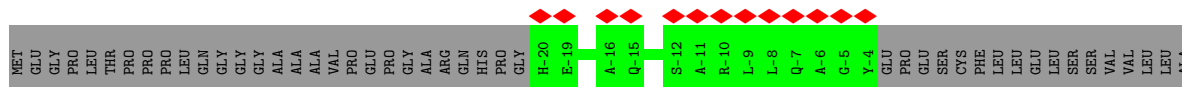
- Molecule 1: Isoform 5 of Inosine-5'-monophosphate dehydrogenase 1

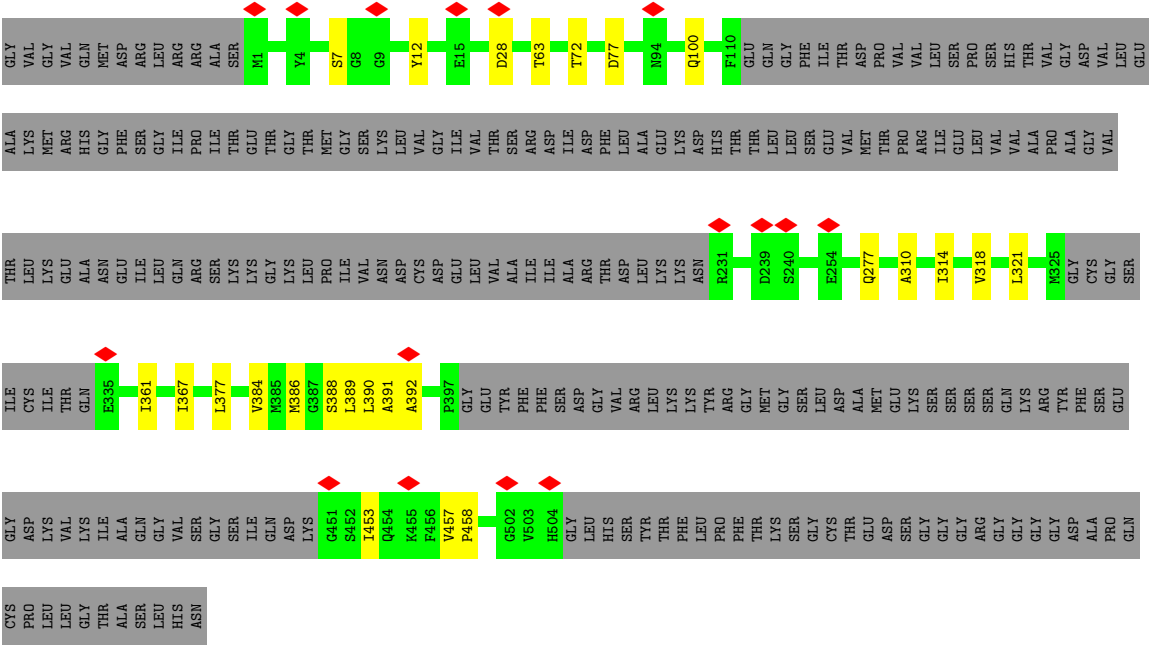


- Molecule 1: Isoform 5 of Inosine-5'-monophosphate dehydrogenase 1



- Molecule 1: Isoform 5 of Inosine-5'-monophosphate dehydrogenase 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60900	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.164	Depositor
Minimum map value	-6.099	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.240	Depositor
Recommended contour level	1.52	Depositor
Map size ($\text{\AA}$)	336.0, 336.0, 336.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.05, 1.05, 1.05	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.73	1/2588 (0.0%)	1.31	4/3494 (0.1%)
1	B	0.72	0/2588	1.31	5/3494 (0.1%)
1	C	0.71	0/2588	1.26	1/3494 (0.0%)
1	D	0.72	0/2588	1.25	3/3494 (0.1%)
1	E	0.72	0/2588	1.30	2/3494 (0.1%)
1	F	0.72	0/2588	1.32	2/3494 (0.1%)
1	G	0.73	0/2588	1.31	2/3494 (0.1%)
1	H	0.72	0/2588	1.26	4/3494 (0.1%)
All	All	0.72	1/20704 (0.0%)	1.29	23/27952 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	273	LEU	C-O	-6.00	1.16	1.24

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	277	GLN	OE1-CD-NE2	-6.31	116.29	122.60
1	D	28	ASP	CA-CB-CG	6.07	118.67	112.60
1	E	28	ASP	CA-CB-CG	5.75	118.35	112.60
1	C	28	ASP	CA-CB-CG	5.62	118.22	112.60
1	E	77	ASP	CA-CB-CG	5.58	118.18	112.60
1	F	77	ASP	CA-CB-CG	5.51	118.11	112.60
1	H	28	ASP	CA-CB-CG	5.45	118.05	112.60
1	G	77	ASP	CA-CB-CG	5.38	117.98	112.60
1	G	28	ASP	CA-CB-CG	5.29	117.89	112.60
1	D	77	ASP	CA-CB-CG	5.24	117.84	112.60
1	A	28	ASP	CA-CB-CG	5.22	117.82	112.60
1	B	355	ARG	NE-CZ-NH2	5.21	123.89	119.20
1	H	77	ASP	CA-CB-CG	5.18	117.78	112.60
1	D	-20	HIS	CB-CG-CD2	-5.17	124.48	131.20
1	H	7	SER	N-CA-C	5.17	116.50	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	355	ARG	NE-CZ-NH2	5.13	123.82	119.20
1	B	77	ASP	CA-CB-CG	5.10	117.70	112.60
1	B	354	ALA	CA-C-N	5.08	127.59	120.28
1	B	354	ALA	C-N-CA	5.08	127.59	120.28
1	A	77	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	100	GLN	OE1-CD-NE2	-5.01	117.59	122.60
1	A	355	ARG	NE-CZ-NH2	5.01	123.71	119.20
1	H	100	GLN	OE1-CD-NE2	-5.01	117.59	122.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2550	2575	2576	3	0
1	B	2550	2575	2576	2	0
1	C	2550	2575	2576	20	0
1	D	2550	2575	2576	19	0
1	E	2550	2575	2576	4	0
1	F	2550	2575	2576	2	0
1	G	2550	2575	2576	2	0
1	H	2550	2575	2576	15	0
All	All	20400	20600	20608	67	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:457:VAL:HG22	1:D:458:PRO:HD3	1.55	0.88
1:H:457:VAL:HG22	1:H:458:PRO:HD3	1.56	0.88
1:C:457:VAL:HG22	1:C:458:PRO:HD3	1.55	0.88
1:H:390:LEU:HD22	1:H:453:ILE:HD11	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:390:LEU:HD22	1:D:453:ILE:HD11	1.64	0.80
1:C:390:LEU:HD22	1:C:453:ILE:HD11	1.64	0.80
1:C:386:MET:HE2	1:C:386:MET:HA	1.69	0.74
1:D:386:MET:HA	1:D:386:MET:HE2	1.70	0.73
1:C:457:VAL:CG2	1:C:458:PRO:HD3	2.23	0.68
1:H:457:VAL:CG2	1:H:458:PRO:HD3	2.24	0.68
1:D:457:VAL:CG2	1:D:458:PRO:HD3	2.24	0.68
1:C:321:LEU:HB2	1:C:361:ILE:HD13	1.79	0.64
1:H:321:LEU:HB2	1:H:361:ILE:HD13	1.78	0.64
1:E:321:LEU:HB2	1:E:361:ILE:HD13	1.79	0.64
1:D:321:LEU:HB2	1:D:361:ILE:HD13	1.78	0.64
1:C:384:VAL:HG12	1:C:386:MET:HE3	1.82	0.61
1:D:384:VAL:HG12	1:D:386:MET:HE3	1.80	0.61
1:C:370:VAL:HG22	1:C:460:LEU:HD22	1.85	0.58
1:D:370:VAL:HG22	1:D:460:LEU:HD22	1.85	0.57
1:H:386:MET:HA	1:H:386:MET:HE2	1.87	0.56
1:H:384:VAL:HG12	1:H:386:MET:HE3	1.88	0.56
1:H:390:LEU:HD22	1:H:453:ILE:CD1	2.34	0.56
1:D:390:LEU:HD22	1:D:453:ILE:CD1	2.34	0.55
1:C:390:LEU:HD22	1:C:453:ILE:CD1	2.35	0.54
1:D:321:LEU:HB2	1:D:361:ILE:CD1	2.38	0.53
1:C:321:LEU:HB2	1:C:361:ILE:CD1	2.39	0.53
1:E:321:LEU:HB2	1:E:361:ILE:CD1	2.38	0.52
1:H:321:LEU:HB2	1:H:361:ILE:CD1	2.38	0.52
1:H:367:ILE:HG21	1:H:386:MET:HE1	1.91	0.52
1:D:337:MET:SD	1:D:337:MET:N	2.84	0.51
1:D:391:ALA:O	1:D:392:ALA:HB3	2.11	0.51
1:H:391:ALA:O	1:H:392:ALA:HB3	2.11	0.51
1:C:391:ALA:O	1:C:392:ALA:HB3	2.11	0.51
1:C:367:ILE:HG21	1:C:386:MET:HE1	1.92	0.50
1:D:310:ALA:O	1:D:314:ILE:HG13	2.13	0.49
1:C:310:ALA:O	1:C:314:ILE:HG13	2.13	0.49
1:H:388:SER:O	1:H:391:ALA:N	2.46	0.48
1:F:388:SER:O	1:F:391:ALA:N	2.46	0.48
1:H:310:ALA:O	1:H:314:ILE:HG13	2.13	0.48
1:D:388:SER:O	1:D:391:ALA:N	2.46	0.48
1:D:386:MET:HE2	1:D:386:MET:CA	2.42	0.47
1:C:386:MET:HE2	1:C:386:MET:CA	2.41	0.46
1:D:367:ILE:HG21	1:D:386:MET:HE1	1.97	0.45
1:D:389:LEU:N	1:D:389:LEU:HD23	2.32	0.44
1:H:389:LEU:N	1:H:389:LEU:HD23	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:VAL:O	1:D:336:VAL:HG23	2.18	0.43
1:H:72:THR:HG22	1:H:72:THR:O	2.19	0.43
1:G:388:SER:O	1:G:391:ALA:N	2.52	0.43
1:C:460:LEU:HD23	1:C:460:LEU:HA	1.80	0.43
1:E:388:SER:O	1:E:391:ALA:N	2.51	0.43
1:C:388:SER:O	1:C:389:LEU:C	2.63	0.42
1:A:388:SER:O	1:A:391:ALA:N	2.52	0.42
1:C:388:SER:O	1:C:391:ALA:N	2.53	0.42
1:H:388:SER:O	1:H:389:LEU:C	2.61	0.42
1:A:72:THR:HG22	1:A:72:THR:O	2.20	0.42
1:D:72:THR:HG22	1:D:72:THR:O	2.20	0.42
1:B:388:SER:O	1:B:391:ALA:N	2.53	0.41
1:A:336:VAL:O	1:A:336:VAL:HG23	2.19	0.41
1:D:388:SER:O	1:D:389:LEU:C	2.62	0.41
1:F:72:THR:O	1:F:72:THR:HG22	2.21	0.41
1:B:72:THR:O	1:B:72:THR:HG22	2.21	0.41
1:C:389:LEU:N	1:C:389:LEU:HD23	2.34	0.41
1:C:72:THR:HG22	1:C:72:THR:O	2.20	0.41
1:E:72:THR:HG22	1:E:72:THR:O	2.21	0.41
1:G:72:THR:HG22	1:G:72:THR:O	2.21	0.41
1:C:390:LEU:O	1:C:393:THR:HG23	2.21	0.41
1:C:361:ILE:HD13	1:C:361:ILE:HA	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	329/621 (53%)	317 (96%)	11 (3%)	1 (0%)	36	60
1	B	329/621 (53%)	317 (96%)	11 (3%)	1 (0%)	36	60
1	C	329/621 (53%)	313 (95%)	15 (5%)	1 (0%)	36	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	329/621 (53%)	314 (95%)	14 (4%)	1 (0%)	36 60
1	E	329/621 (53%)	316 (96%)	12 (4%)	1 (0%)	36 60
1	F	329/621 (53%)	317 (96%)	11 (3%)	1 (0%)	36 60
1	G	329/621 (53%)	316 (96%)	12 (4%)	1 (0%)	36 60
1	H	329/621 (53%)	314 (95%)	14 (4%)	1 (0%)	36 60
All	All	2632/4968 (53%)	2524 (96%)	100 (4%)	8 (0%)	37 60

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	TYR
1	B	12	TYR
1	C	12	TYR
1	D	12	TYR
1	E	12	TYR
1	F	12	TYR
1	G	12	TYR
1	H	12	TYR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	267/496 (54%)	261 (98%)	6 (2%)	45 74
1	B	267/496 (54%)	261 (98%)	6 (2%)	45 74
1	C	267/496 (54%)	262 (98%)	5 (2%)	50 77
1	D	267/496 (54%)	263 (98%)	4 (2%)	57 81
1	E	267/496 (54%)	262 (98%)	5 (2%)	50 77
1	F	267/496 (54%)	261 (98%)	6 (2%)	45 74
1	G	267/496 (54%)	261 (98%)	6 (2%)	45 74
1	H	267/496 (54%)	263 (98%)	4 (2%)	57 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2136/3968 (54%)	2094 (98%)	42 (2%)	48 76

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	THR
1	A	277	GLN
1	A	318	VAL
1	A	377	LEU
1	A	388	SER
1	A	496	SER
1	B	63	THR
1	B	318	VAL
1	B	339	CYS
1	B	377	LEU
1	B	388	SER
1	B	496	SER
1	C	63	THR
1	C	277	GLN
1	C	318	VAL
1	C	377	LEU
1	C	388	SER
1	D	63	THR
1	D	277	GLN
1	D	318	VAL
1	D	377	LEU
1	E	63	THR
1	E	277	GLN
1	E	318	VAL
1	E	377	LEU
1	E	388	SER
1	F	63	THR
1	F	277	GLN
1	F	318	VAL
1	F	339	CYS
1	F	377	LEU
1	F	496	SER
1	G	63	THR
1	G	277	GLN
1	G	318	VAL
1	G	377	LEU
1	G	388	SER

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Mol	Chain	Res	Type
1	G	495	MET
1	H	63	THR
1	H	277	GLN
1	H	318	VAL
1	H	377	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	288	HIS
1	B	33	ASN
1	B	243	GLN
1	B	288	HIS
1	C	33	ASN
1	C	243	GLN
1	C	288	HIS
1	C	303	ASN
1	D	33	ASN
1	D	288	HIS
1	D	296	HIS
1	D	303	ASN
1	E	288	HIS
1	E	296	HIS
1	F	288	HIS
1	G	33	ASN
1	G	283	GLN
1	G	288	HIS
1	G	303	ASN
1	H	288	HIS
1	H	303	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

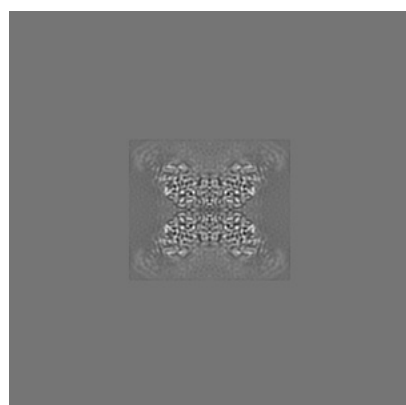
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24440. These allow visual inspection of the internal detail of the map and identification of artifacts.

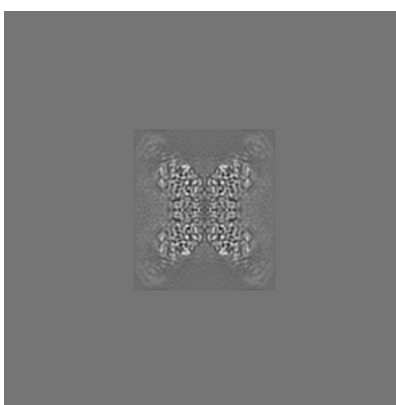
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

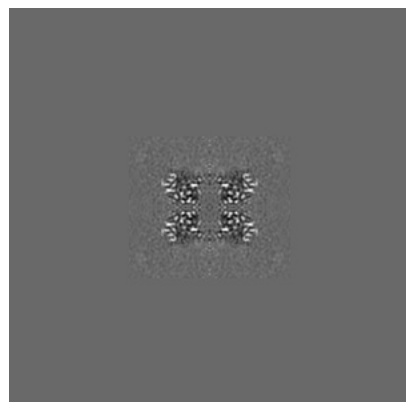


Z

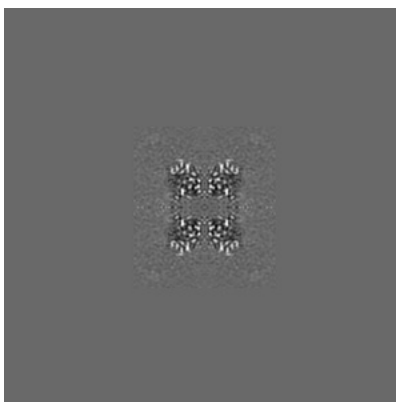
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

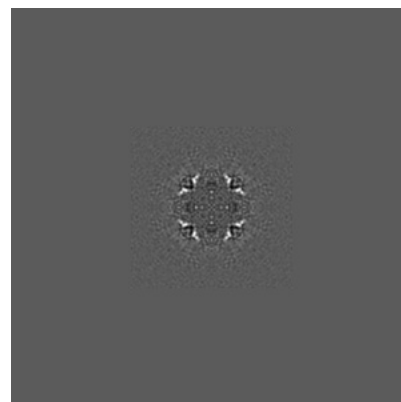
6.2.1 Primary map



X Index: 160



Y Index: 160

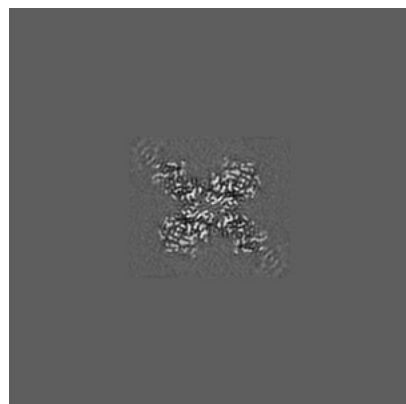


Z Index: 160

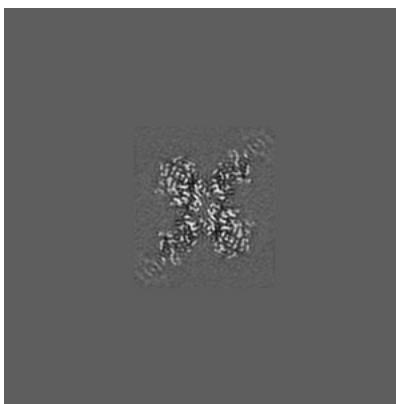
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

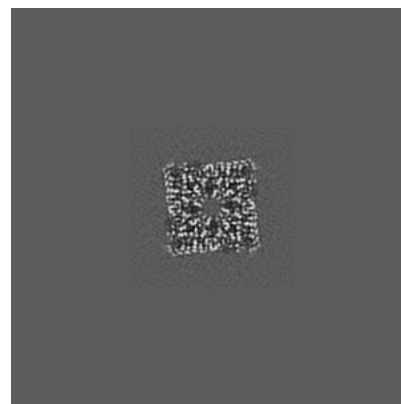
6.3.1 Primary map



X Index: 183



Y Index: 183

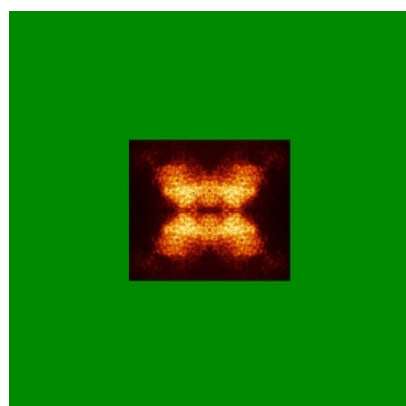


Z Index: 174

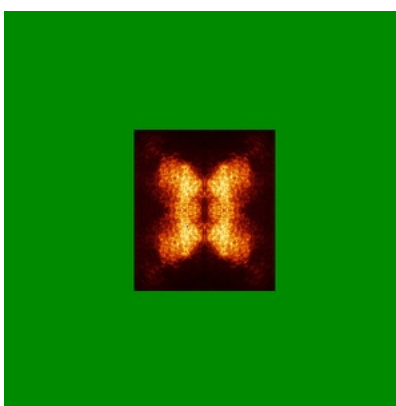
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

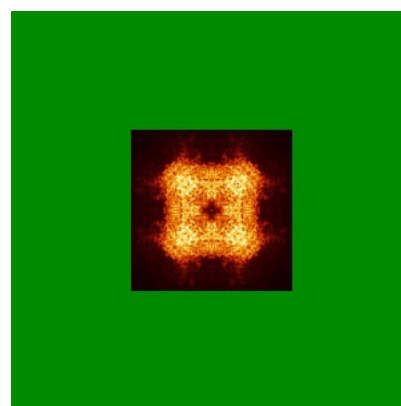
6.4.1 Primary map



X



Y

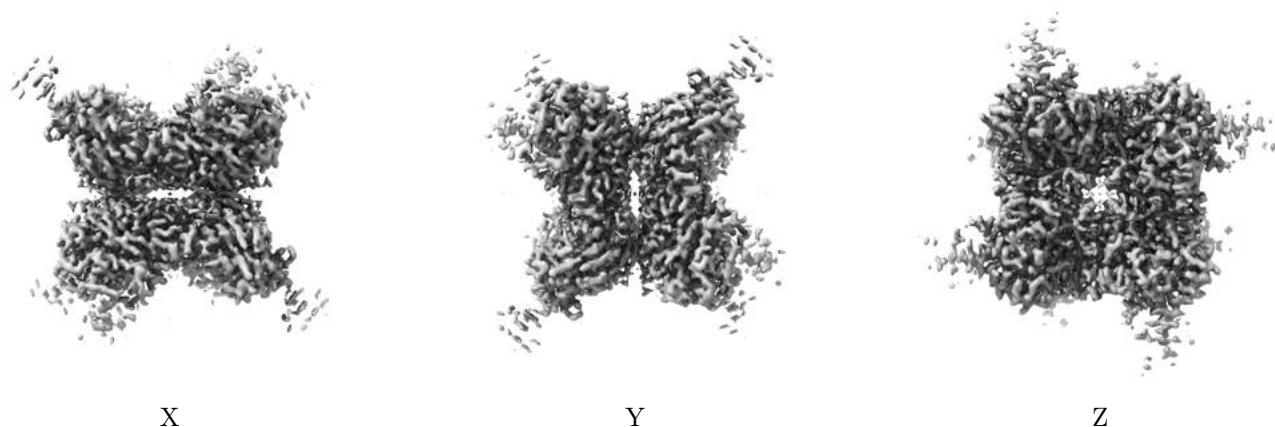


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.52. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

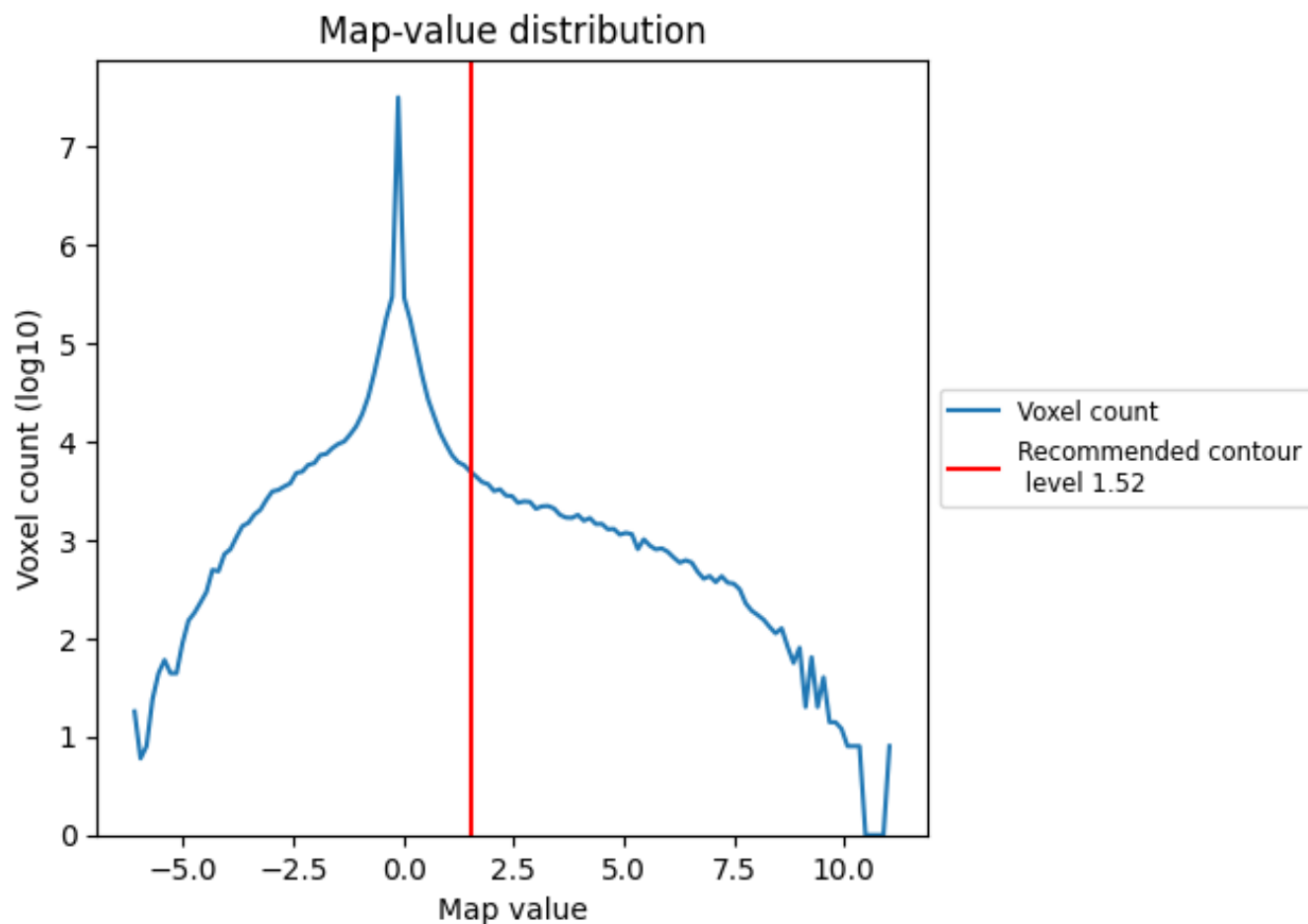
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

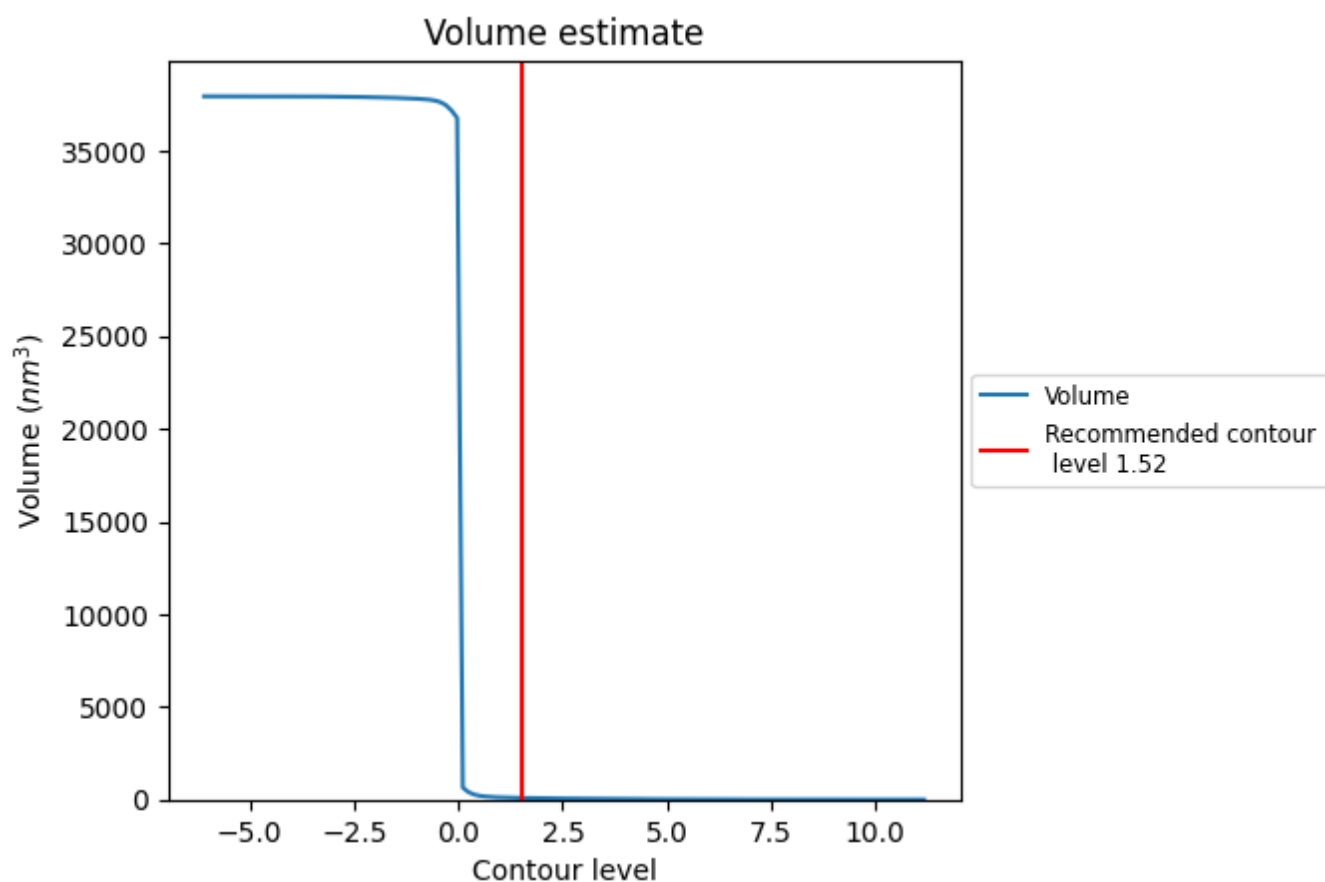
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

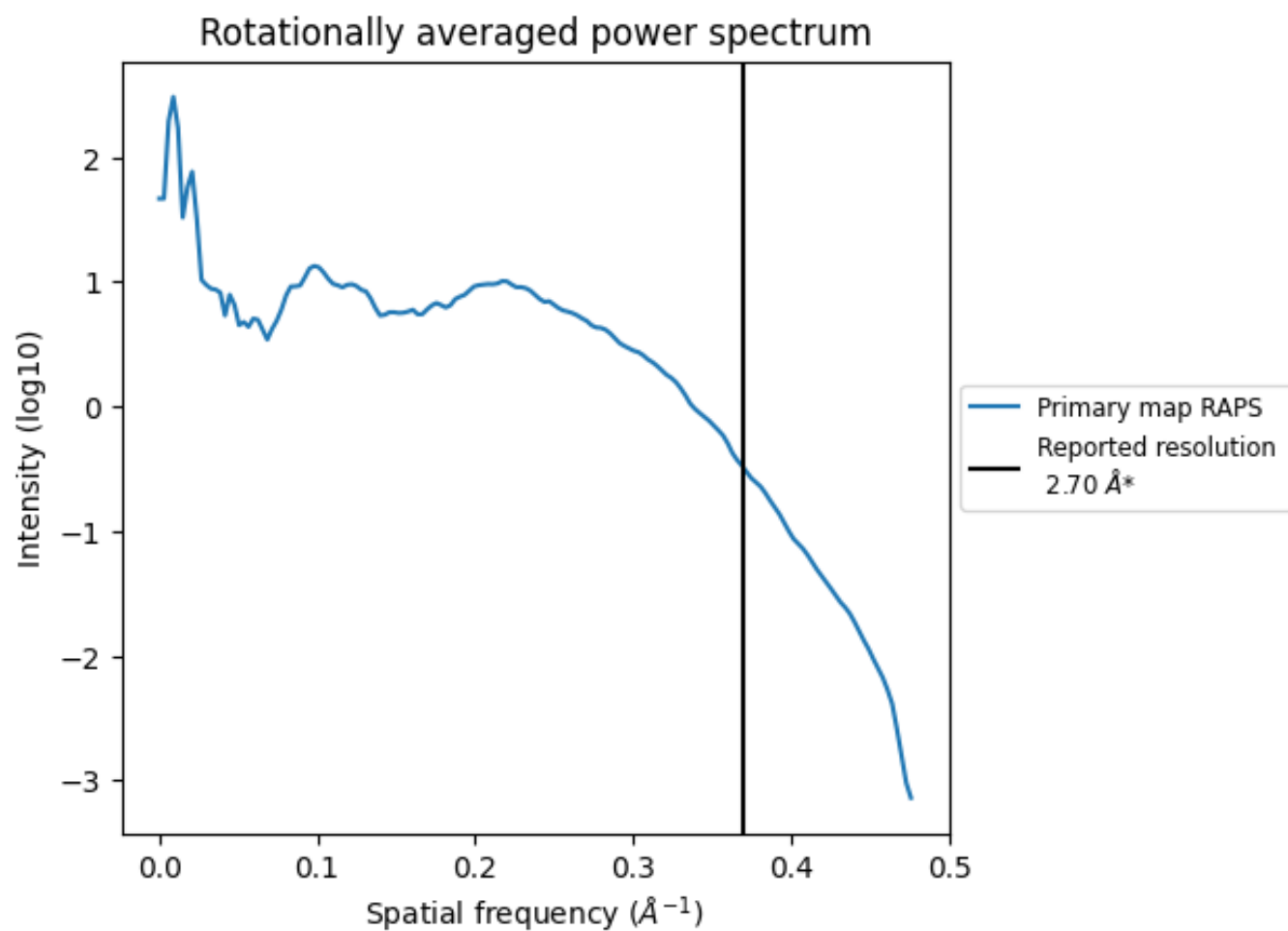
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 88 nm^3 ; this corresponds to an approximate mass of 79 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

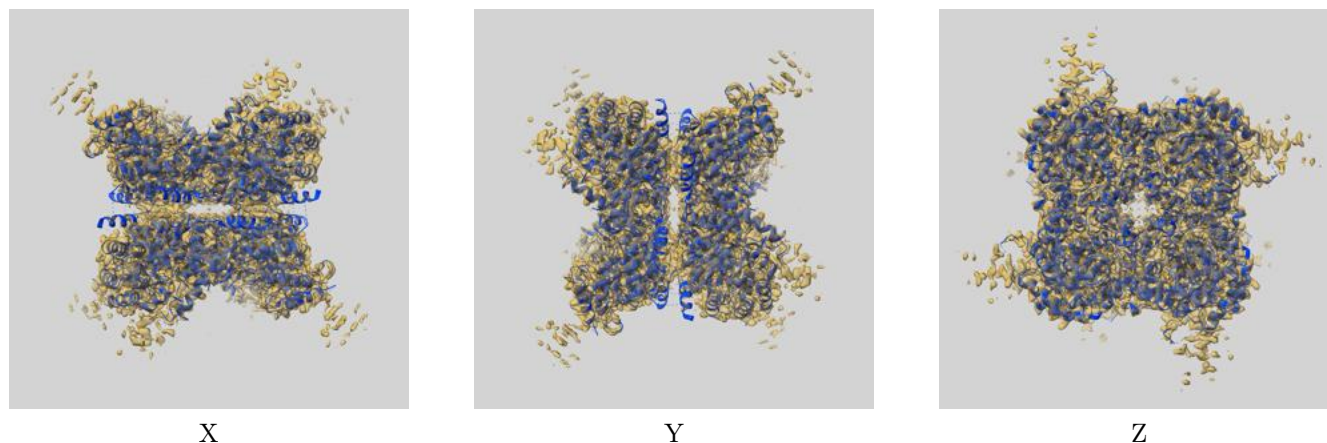
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

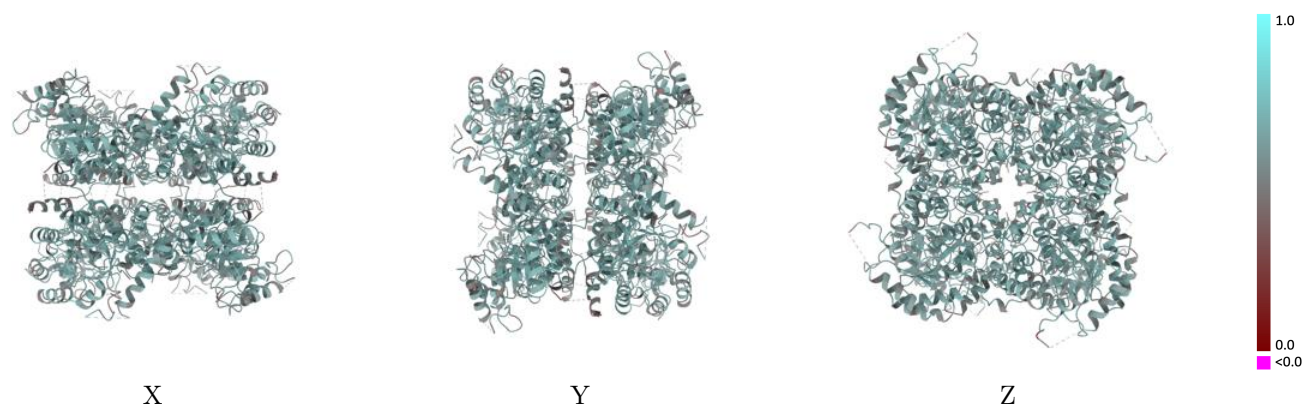
This section contains information regarding the fit between EMDB map EMD-24440 and PDB model 7RFF. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



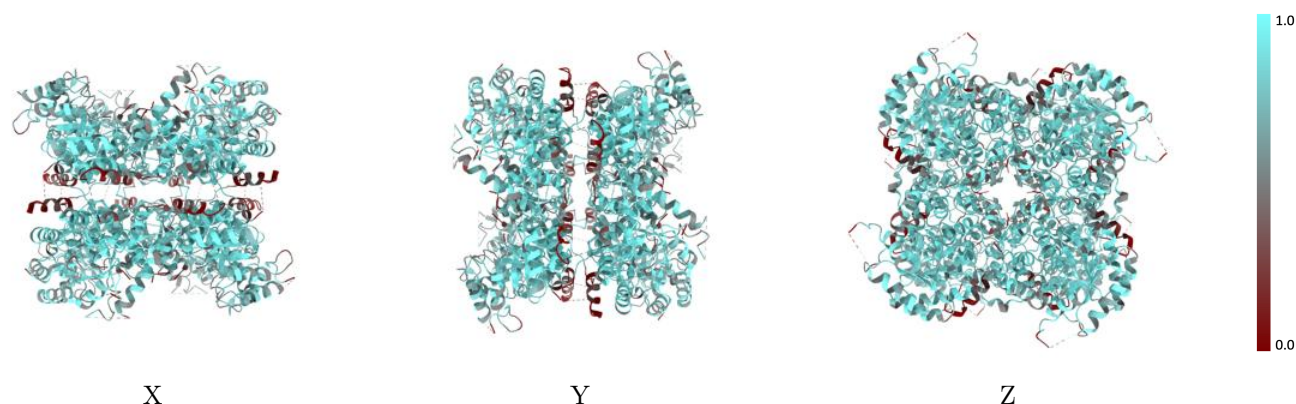
The images above show the 3D surface view of the map at the recommended contour level 1.52 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



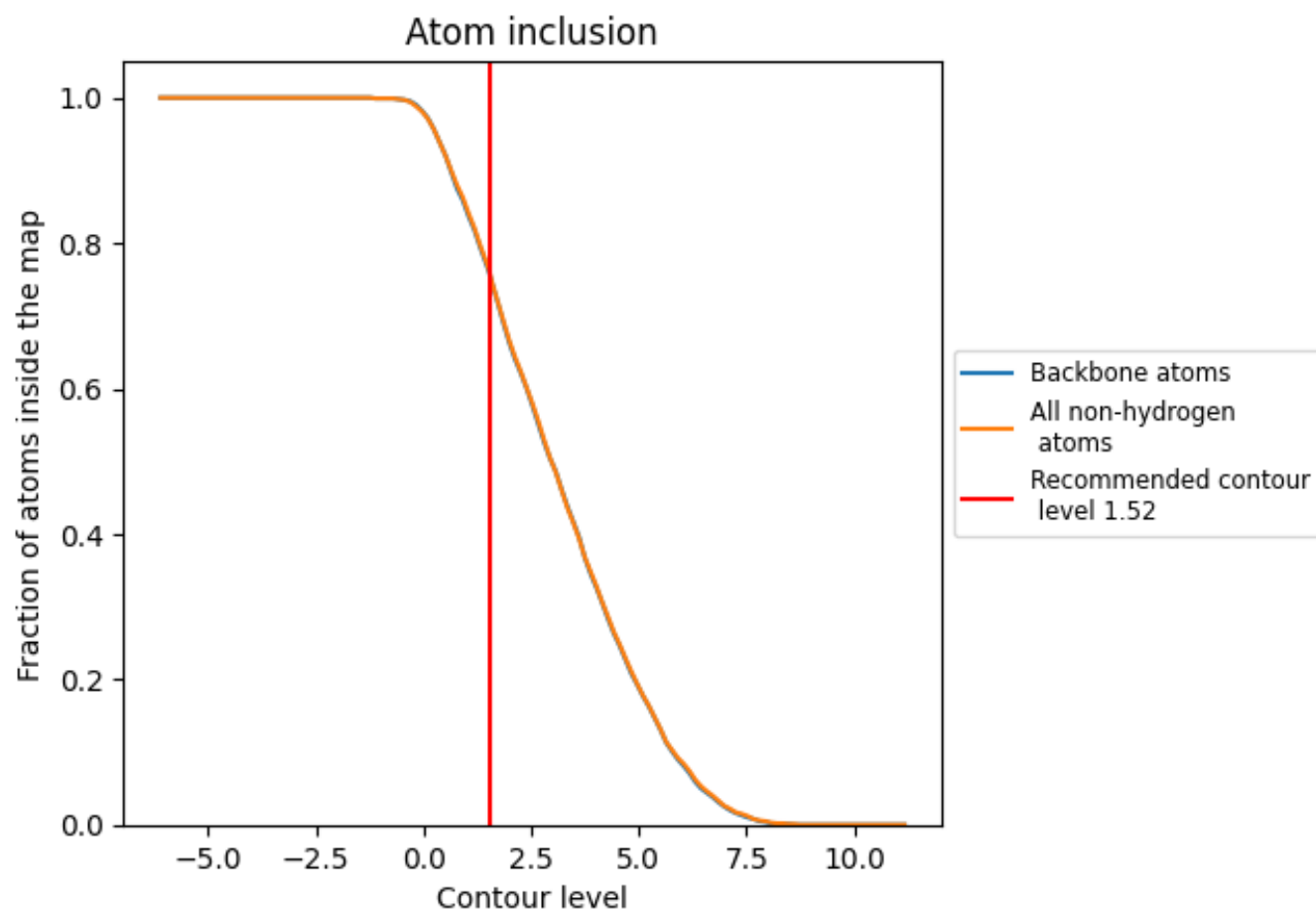
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.52).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.52) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7640	0.5980
A	0.7750	0.5990
B	0.7750	0.5980
C	0.7740	0.5980
D	0.7750	0.6000
E	0.7730	0.6000
F	0.7720	0.5980
G	0.7720	0.5960
H	0.7730	0.5980

1.0

0.0

<0.0